

In the claims:

1. (currently amended) A method of quantitatively analyzing a sample analyte, comprising:

performing matrix-assisted laser desorption ionization mass spectrometry on the sample analyte and an internal standard, and comparing signal intensities~~the mass spectrometry~~ of the sample analyte with signal intensities~~the mass spectrometry~~ of the internal standard without the use of calibration curves, wherein the sample analyte and the internal standard are compared according to the following equation:

$$(MW(\text{Sample}) \times \sum I(\text{Sample})) / [\text{Sample}] = (MW(\text{IS}) \times \sum I(\text{IS})) / [\text{IS}]$$

where MW designates molecular weight, $\sum I$ designates sum of peak intensities, brackets designate concentration, and IS designates internal standard.

2. (canceled)

3. (original) The method of claim 1, wherein the sample analyte is a biomolecule.

4. The method of claim 3, wherein the sample analyte is selected from peptides, proteins and digest fragments of sample peptide or sample protein.

5. The method of claim 3, wherein the sample analyte is selected from DNA, t-RNA, m-RNA or r-RNA or sample digest fragments.

6. (canceled)

7. (original) The method of claim 1, wherein the internal standard is selected from a biomolecule and a synthetic molecule.

8. (canceled).

9. (currently amended) The method of claim 18, wherein the sample analyte and the internal standard are each a biomolecule that ionizes, upon application of the matrix-assisted laser desorption ionization, primarily on a same functional group.

10. (currently amended) A method of quantitatively analyzing a sample analyte, comprising:

performing matrix-assisted laser desorption ionization mass spectrometry on the sample analyte and an internal standard, and comparing signal intensities of the sample analyte with signal intensities of the internal standard~~The method of claim 2~~, wherein the sample analyte and the internal standard are compared according to the following equation:

$$(MW(\text{Sample}) \times \sum I(\text{Sample})) / [\text{Sample}] = (MW(\text{IS}) \times \sum I(\text{IS})) / [\text{IS}] * C$$

where MW designates molecular weight, ΣI designates sum of peak intensities, I designates peak intensity, brackets designate concentration, and IS designates internal standard and C represent a constant.

11. (original) The method of claim 10, wherein the sample analyte and the internal standard are each proteins that ionize, upon application of the matrix-assisted laser desorption ionization, on different functional group where the constant C corrects for ionization efficiencies.

12. (original) The method of claim 1, wherein matrix-assisted laser desorption ionization time-of-flight mass spectrometry is performed on the sample analyte.

Claims 13-26 (canceled)